



# SEQUENCE LISTING

<110> FUJIWARA, TSUTOMU  
WATANABE, TAKESHI  
HORIE, MASATO

<120> HUMAN SKELETAL MUSCLE-SPECIFIC  
UMBIQUITIN-CONJUGATING ENZYME

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<141> 2004-02-20

<150> 10/342,276

<151> 2003-01-15

<150> 09/273,565

<151> 1999-03-22

<150> 09/055,699

<151> 1998-04-07

<150> 08/820,170

<151> 1997-03-19

<150> JP 63410/1996

<151> 1996-03-19

<150> JP 69163/1997

<151> 1997-03-05

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<170> PatentIn Ver. 2.1

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Pro Gly Glu Arg Glu Leu Thr Ile Pro Ala Ser Ala Asn Val Phe Tyr	50	55	60		
Pro Met Asp Gly Ala Ser His Asp Phe Leu Leu Arg Gln Arg Arg Arg	65	70	75	80	
Ser Ser Thr Ala Thr Pro Gly Val Thr Ser Gly Pro Ser Ala Ser Gly	85	90	95		
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tat gag ctg gta cag ctg cta cca ggg gag cga gag ctg act atc cca 198  
Tyr Glu Leu Val Gln Leu Leu Pro Gly Glu Arg Glu Leu Thr Ile Pro  
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gcc tcg gct aat gta ttc tac ccc atg gat gga gct tca cac gat ttc 246  
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ctc ctg cgg cag cgg cga agg tcc tct act gct aca cct ggc gtc acc 294  
Leu Leu Arg Gln Arg Arg Arg Ser Ser Thr Ala Thr Pro Gly Val Thr  
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Ser Gly Pro Ser Ala Ser Gly Thr Pro Pro Ser Glu Gly Gly Gly Gly  
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Ser Phe Leu Lys Arg Ser Lys Leu Gly Arg Tyr Asn Glu Glu Glu Arg  
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Val	Thr	Ile	Lys	Glu	Gly	Ser	Gln	Leu	Lys	Gln	Gln	Ile	Gln	Ser	Ile		
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Ala Val Gly Tyr His Ile Pro Asn Pro Glu Val Ile Phe Arg Met Leu  
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 Met Pro Ala Asp

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Gly Lys Val Phe Ile Gln Arg Ser Glu Leu Leu Thr His Gln Lys Thr	
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Glu Leu Ile Thr His Gln Arg Thr His Met Gly Glu Lys Pro Tyr Glu	
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Tyr	Ala	Arg	Asp	His	Gln	Pro	Cys	Ile	Ile	Phe	Met	Asp	Glu	Ile	Asp	
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gct	att	ggc	ggc	cgt	cgg	ttt	tct	gag	ggc	act	tca	gct	gac	aga	gag	772



Ala	Ile	Gly	Gly	Arg	Arg	Phe	Ser	Glu	Gly	Thr	Ser	Ala	Asp	Arg	Glu	
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Ile	Gln	Arg	Thr	Leu	Met	Glu	Leu	Leu	Asn	Gln	Met	Asp	Gly	Phe	Asp	
		255					260					265				
act	ctg	cat	aga	gtt	aaa	atg	acc	atg	gct	aca	aac	aga	cca	gat	aca	868
Thr	Leu	His	Arg	Val	Lys	Met	Thr	Met	Ala	Thr	Asn	Arg	Pro	Asp	Thr	
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ctg	gat	cct	gct	ttg	ctg	cgt	cca	gga	aga	tta	gat	aga	aaa	ata	cat	916
Leu	Asp	Pro	Ala	Leu	Leu	Arg	Pro	Gly	Arg	Leu	Asp	Arg	Lys	Ile	His	
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att	gat	ttg	cca	aat	gaa	caa	gca	aga	tta	gac	ata	ctg	aaa	atc	cat	964
Ile	Asp	Leu	Pro	Asn	Glu	Gln	Ala	Arg	Leu	Asp	Ile	Leu	Lys	Ile	His	
				305					310					315		
gca	ggt	ccc	att	aca	aag	cat	ggt	gaa	ata	gat	tat	gaa	gca	att	gtg	1012
Ala	Gly	Pro	Ile	Thr	Lys	His	Gly	Glu	Ile	Asp	Tyr	Glu	Ala	Ile	Val	
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Lys	Leu	Ser	Asp	Gly	Phe	Asn	Gly	Ala	Asp	Leu	Arg	Asn	Val	Cys	Thr	
		335					340					345				
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Glu	Ala	Gly	Met	Phe	Ala	Ile	Arg	Ala	Asp	His	Asp	Phe	Val	Val	Gln	
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Glu	Asp	Phe	Met	Lys	Ala	Val	Arg	Lys	Val	Ala	Asp	Ser	Lys	Lys	Leu	
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Glu	Ser	Lys	Leu	Asp	Tyr	Lys	Pro	Val								
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cagcaagtta caaagggaaa gtgttgaagc ttttcatatt tgctgcgtga gcattttgta																1443

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 <213> Homo sapiens

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 35 40 45  
 Gly Ile Gly Met Asn Glu Pro Leu Val Asp Cys Glu Gly Tyr Pro Arg  
 50 55 60  
 Ser Asp Val Asp Leu Tyr Gln Val Arg Thr Ala Arg His Asn Ile Ile  
 65 70 75 80  
 Cys Leu Gln Asn Asp His Lys Ala Val Met Lys Gln Val Glu Glu Ala  
 85 90 95  
 Leu His Gln Leu His Ala Arg Asp Lys Glu Lys Gln Ala Arg Asp Met  
 100 105 110  
 Ala Glu Ala His Lys Glu Ala Met Ser Arg Lys Leu Gly Gln Ser Glu  
 115 120 125  
 Ser Gln Gly Pro Pro Arg Ala Phe Ala Lys Val Asn Ser Ile Ser Pro  
 130 135 140  
 Gly Ser Pro Ala Ser Ile Ala Gly Leu Gln Val Asp Asp Glu Ile Val  
 145 150 155 160  
 Glu Phe Gly Ser Val Asn Thr Gln Asn Phe Gln Ser Leu His Asn Ile  
 165 170 175

Gly	Ser	Val	Val	Gln	His	Ser	Glu	Gly	Lys	Pro	Leu	Asn	Val	Thr	Val
			180					185					190		
Ile	Arg	Arg	Gly	Glu	Lys	His	Gln	Leu	Arg	Leu	Val	Pro	Thr	Arg	Trp
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 cacgctcgcg acaaggagaa gcaggcccgg gacatggctg aggcccacia agaggccatg 360  
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 gagttcggct ctgtgaacac ccagaacttc cagtcactgc ataacattgg cagtgtggtg 540  
 cagcacagtg aggggaagcc cctgaatgtg acagtgatcc gcagggggga aaaacaccag 600  
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cacg atg tcc gac gag gaa gcg agg cag agc gga ggc tcc tcg cag gcc 169

Met Ser Asp Glu Glu Ala Arg Gln Ser Gly Gly Ser Ser Gln Ala

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5

10

15

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Gly Val Val Thr Val Ser Asp Val Gln Glu Leu Met Arg Arg Lys Glu

20

25

30

gag ata gaa gcg cag atc aag gcc aac tat gac gtg ctg gaa agc caa 265

Glu Ile Glu Ala Gln Ile Lys Ala Asn Tyr Asp Val Leu Glu Ser Gln

35

40

45

aaa ggc att ggg atg aac gag ccg ctg gtg gac tgt gag ggc tac ccc 313

Lys Gly Ile Gly Met Asn Glu Pro Leu Val Asp Cys Glu Gly Tyr Pro

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55

60

cgg tca gac gtg gac ctg tac caa gtc cgc acc gcc agg cac aac atc 361

Arg Ser Asp Val Asp Leu Tyr Gln Val Arg Thr Ala Arg His Asn Ile

65

70

75

ata tgc ctg cag aat gat cac aag gca gtg atg aag cag gtg gag gag 409

Ile Cys Leu Gln Asn Asp His Lys Ala Val Met Lys Gln Val Glu Glu

80

85

90

95

gcc ctg cac cag ctg cac gct cgc gac aag gag aag cag gcc cgg gac 457

Ala Leu His Gln Leu His Ala Arg Asp Lys Glu Lys Gln Ala Arg Asp

100

105

110

atg gct gag gcc cac aaa gag gcc atg agc cgc aaa ctg ggt cag agt 505

Met Ala Glu Ala His Lys Glu Ala Met Ser Arg Lys Leu Gly Gln Ser

115

120

125

gag agc cag ggc cct cca cgg gcc ttc gcc aaa gtg aac agc atc agc 553

Glu Ser Gln Gly Pro Pro Arg Ala Phe Ala Lys Val Asn Ser Ile Ser

130

135

140

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Pro Gly Ser Pro Ala Ser Ile Ala Gly Leu Gln Val Asp Asp Glu Ile	
145 150 155	
gtg gag ttc ggc tct gtg aac acc cag aac ttc cag tca ctg cat aac	649
Val Glu Phe Gly Ser Val Asn Thr Gln Asn Phe Gln Ser Leu His Asn	
160 165 170 175	
att ggc agt gtg gtg cag cac agt gag ggg aag ccc ctg aat gtg aca	697
Ile Gly Ser Val Val Gln His Ser Glu Gly Lys Pro Leu Asn Val Thr	
180 185 190	
gtg atc cgc agg ggg gaa aaa cac cag ctt aga ctt gtt cca aca cgc	745
Val Ile Arg Arg Gly Glu Lys His Gln Leu Arg Leu Val Pro Thr Arg	
195 200 205	
tgg gca gga aaa gga ctg ctg ggc tgc aac att att cct ctg caa aga	793
Trp Ala Gly Lys Gly Leu Leu Gly Cys Asn Ile Ile Pro Leu Gln Arg	
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45

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Pro Glu Pro Ser Arg Arg Ala Arg Arg Ala Pro Leu Gly Thr Asn Phe  
85 90 95

Val Asp Arg Leu Pro Gln Ala Val Arg Asn Arg Val Gln Ala Leu Arg  
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115 120 125

Ile His Asp Leu Glu Arg Lys Tyr Ala Glu Leu Asn Lys Pro Leu Tyr  
130 135 140

Asp Arg Arg Phe Gln Ile Ile Asn Ala Glu Tyr Glu Pro Thr Glu Glu  
145 150 155 160

Glu Cys Glu Trp Asn Ser Glu Asp Glu Glu Phe Ser Ser Asp Glu Glu  
165 170 175

Val Gln Asp Asn Thr Pro Ser Glu Met Pro Pro Leu Glu Gly Glu Glu  
180 185 190

Glu Glu Asn Pro Lys Glu Asn Pro Glu Val Lys Ala Glu Glu Lys Glu  
195 200 205

Val Pro Lys Glu Ile Pro Glu Val Lys Asp Glu Glu Lys Glu Val Ala  
210 215 220

Lys Glu Ile Pro Glu Val Lys Ala Glu Glu Lys Ala Asp Ser Lys Asp  
225 230 235 240

Cys Met Glu Ala Thr Pro Glu Val Lys Glu Asp Pro Lys Glu Val Pro  
245 250 255

Gln Val Lys Ala Asp Asp Lys Glu Gln Pro Lys Ala Thr Glu Ala Lys  
260 265 270

Ala Arg Ala Ala Val Arg Glu Thr His Lys Arg Val Pro Glu Glu Arg  
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Asn	Val	Asp	Lys	Leu	Gly	Pro	Met	Ile	Gln	Lys	Tyr	Asp	Glu	Pro	Ile	325	330	335
Leu	Lys	Phe	Leu	Ser	Asp	Val	Ser	Leu	Lys	Phe	Ser	Lys	Pro	Gly	Gln	340	345	350
Pro	Val	Ser	Tyr	Thr	Phe	Glu	Phe	His	Phe	Leu	Pro	Asn	Pro	Tyr	Phe	355	360	365
Arg	Asn	Glu	Val	Leu	Val	Lys	Thr	Tyr	Ile	Ile	Lys	Ala	Lys	Pro	Asp	370	375	380
His	Asn	Asp	Pro	Phe	Phe	Ser	Trp	Gly	Trp	Glu	Ile	Glu	Asp	Cys	Lys	385	390	395
Gly	Cys	Lys	Ile	Asp	Arg	Arg	Arg	Gly	Lys	Asp	Val	Thr	Val	Thr	Thr	405	410	415
Thr	Gln	Ser	Arg	Thr	Thr	Ala	Thr	Gly	Glu	Ile	Glu	Ile	Gln	Pro	Arg	420	425	430
Val	Val	Pro	Asn	Ala	Ser	Phe	Phe	Asn	Phe	Phe	Ser	Pro	Pro	Glu	Ile	435	440	445
Pro	Met	Ile	Gly	Lys	Leu	Glu	Pro	Arg	Glu	Asp	Ala	Ile	Leu	Asp	Glu	450	455	460
Asp	Phe	Glu	Ile	Gly	Gln	Ile	Leu	His	Asp	Asn	Val	Ile	Leu	Lys	Ser	465	470	475
Ile	Tyr	Tyr	Tyr	Thr	Gly	Glu	Val	Asn	Gly	Thr	Tyr	Tyr	Gln	Phe	Gly	485	490	495
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<211> 1518

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<213> Homo sapiens

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	75					80					85					
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	90				95					100					105	
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				110					115					120		
gat Asp	acc Thr	ctg Leu	ttc Phe	tta Leu	aaa Lys	gca Ala	att Ile	cat His	gat Asp	ctt Leu	gaa Glu	aga Arg	aaa Lys	tat Tyr	gct Ala	676
			125					130					135			
gaa Glu	ctc Leu	aac Asn	aag Lys	cct Pro	ctg Leu	tat Tyr	gat Asp	agg Arg	cgg Arg	ttt Phe	caa Gln	atc Ile	atc Ile	aat Asn	gca Ala	724
		140					145					150				
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			205				210					215				
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		220					225					230				
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cct aaa gca aca gag gct aag gca agg gct gca gta aga gag act cat Pro Lys Ala Thr Glu Ala Lys Ala Arg Ala Ala Val Arg Glu Thr His 270 275 280			1108
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Phe Phe Ser Pro Pro Glu Ile Pro Met Ile Gly Lys Leu Glu Pro Arg	
445 450 455	
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Lys	
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ccactgaggt gttaatataa catagtattt ttgaaaaagt ttcttcatct tatattgtgt	2493
aattgtaaac taaagatacc gtgttttctt tgtattgtgt tctaccttcc ctttcaactga	2553

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aatattaaag tgtgttatac tat 2636

<210> 22

<211> 170

<212> PRT

<213> Homo sapiens

<400> 22

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			20					25					30		

Asn	Asp	Leu	Tyr	Arg	Trp	Glu	Val	Leu	Ile	Ile	Gly	Pro	Pro	Asp	Thr
		35					40					45			

Leu	Tyr	Glu	Gly	Gly	Val	Phe	Lys	Ala	His	Leu	Thr	Phe	Pro	Lys	Asp
	50					55					60				

Tyr	Pro	Leu	Arg	Pro	Pro	Lys	Met	Lys	Phe	Ile	Thr	Glu	Ile	Trp	His
65					70					75					80

Pro	Asn	Val	Asp	Lys	Asn	Gly	Asp	Val	Cys	Ile	Ser	Ile	Leu	His	Glu
				85					90					95	

Pro	Gly	Glu	Asp	Lys	Tyr	Gly	Tyr	Glu	Lys	Pro	Glu	Glu	Arg	Trp	Leu
			100					105					110		

Pro	Ile	His	Thr	Val	Glu	Thr	Ile	Met	Ile	Ser	Val	Ile	Ser	Met	Leu
		115					120					125			

Ala	Asp	Pro	Asn	Gly	Asp	Ser	Pro	Ala	Asn	Val	Asp	Ala	Ala	Lys	Glu
	130					135					140				

Trp	Arg	Glu	Asp	Arg	Asn	Gly	Glu	Phe	Lys	Arg	Lys	Val	Ala	Arg	Cys
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Val	Arg	Lys	Ser	Gln	Glu	Thr	Ala	Phe	Glu
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<210> 23

<211> 510  
<212> DNA  
<213> Homo sapiens

<400> 23  
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cttattattg gccctccaga tacactttat gaagggtggtg tttttaaggc tcattcttact 180  
ttcccaaaag attatcccct ccgacctcct aaaatgaaat tcattacaga aatctggcac 240  
ccaaatgttg ataaaaatgg tgatgtgtgc atttctattc ttcatgagcc tggggaagat 300  
aagtatgggtt atgaaaagcc agaggaacgc tggctcccta tccacactgt ggaaaccatc 360  
atgattagtg tcattttctat gctggcagac cctaattggag actcacctgc taatgttgat 420  
gctgcgaaag aatggaggga agatagaaat ggagaattta aaagaaaagt tgcccgtctg 480  
gtaagaaaaa gccaaagagac tgcttttgag 510

<210> 24  
<211> 617  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (19)..(528)

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1 5 10  
aga cag ctg gca gaa ctc aac aaa aat cca gtg gaa ggc ttt tct gca 99  
Arg Gln Leu Ala Glu Leu Asn Lys Asn Pro Val Glu Gly Phe Ser Ala  
15 20 25  
ggt tta ata gat gac aat gat ctc tac cga tgg gaa gtc ctt att att 147  
Gly Leu Ile Asp Asp Asn Asp Leu Tyr Arg Trp Glu Val Leu Ile Ile  
30 35 40

ggc	cct	cca	gat	aca	ctt	tat	gaa	ggt	ggt	gtt	ttt	aag	gct	cat	ctt	195
Gly	Pro	Pro	Asp	Thr	Leu	Tyr	Glu	Gly	Gly	Val	Phe	Lys	Ala	His	Leu	
	45					50					55					

act	ttc	cca	aaa	gat	tat	ccc	ctc	cga	cct	cct	aaa	atg	aaa	ttc	att	243
Thr	Phe	Pro	Lys	Asp	Tyr	Pro	Leu	Arg	Pro	Pro	Lys	Met	Lys	Phe	Ile	
	60				65					70					75	

aca	gaa	atc	tgg	cac	cca	aat	gtt	gat	aaa	aat	ggt	gat	gtg	tgc	att	291
Thr	Glu	Ile	Trp	His	Pro	Asn	Val	Asp	Lys	Asn	Gly	Asp	Val	Cys	Ile	
				80					85					90		

tct	att	ctt	cat	gag	cct	ggg	gaa	gat	aag	tat	ggt	tat	gaa	aag	cca	339
Ser	Ile	Leu	His	Glu	Pro	Gly	Glu	Asp	Lys	Tyr	Gly	Tyr	Glu	Lys	Pro	
			95					100					105			

gag	gaa	cgc	tgg	ctc	cct	atc	cac	act	gtg	gaa	acc	atc	atg	att	agt	387
Glu	Glu	Arg	Trp	Leu	Pro	Ile	His	Thr	Val	Glu	Thr	Ile	Met	Ile	Ser	
		110					115					120				

gtc	att	tct	atg	ctg	gca	gac	cct	aat	gga	gac	tca	cct	gct	aat	gtt	435
Val	Ile	Ser	Met	Leu	Ala	Asp	Pro	Asn	Gly	Asp	Ser	Pro	Ala	Asn	Val	
	125					130					135					

gat	gct	gcg	aaa	gaa	tgg	agg	gaa	gat	aga	aat	gga	gaa	ttt	aaa	aga	483
Asp	Ala	Ala	Lys	Glu	Trp	Arg	Glu	Asp	Arg	Asn	Gly	Glu	Phe	Lys	Arg	
	140				145					150					155	

aaa	gtt	gcc	cgc	tgt	gta	aga	aaa	agc	caa	gag	act	gct	ttt	gag		528
Lys	Val	Ala	Arg	Cys	Val	Arg	Lys	Ser	Gln	Glu	Thr	Ala	Phe	Glu		
				160					165					170		

tgacatttat	ttagcagcta	gtaacttcac	ttattttcagg	gtctccaatt	gagaaacatg	588
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<210> 25  
 <211> 374  
 <212> PRT  
 <213> Homo sapiens

<400> 25
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1 5 10 15





Ser Ala Arg Glu His His Ile Pro Cys Pro Glu His Tyr Asn Gly Phe  
260 265 270

Cys Met His Gly Lys Cys Glu His Ser Ile Asn Met Gln Glu Pro Ser  
275 280 285

Cys Arg Cys Asp Ala Gly Tyr Thr Gly Gln His Cys Glu Lys Lys Asp  
290 295 300

Tyr Ser Val Leu Tyr Val Val Pro Gly Pro Val Arg Phe Gln Tyr Val  
305 310 315 320

Leu Ile Ala Ala Val Ile Gly Thr Ile Gln Ile Ala Val Ile Cys Val  
325 330 335

Val Val Leu Cys Ile Thr Arg Lys Cys Pro Arg Ser Asn Arg Ile His  
340 345 350

Arg Gln Lys Gln Asn Thr Gly His Tyr Ser Ser Asp Asn Thr Thr Arg  
355 360 365

Ala Ser Thr Arg Leu Ile  
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<210> 26

<211> 1122

<212> DNA

<213> Homo sapiens

<400> 26

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ttccctacct ccttaagtga ctgccaaacg cccaccggct ggaattgctc tggttatgat 180  
gacagagaaa atgatctctt cctctgtgac accaacacct gttaaatttga tggggaatgt 240  
ttaagaattg gagacactgt gacttgcgtc tgtcagttca agtgcaacaa tgactatgtg 300  
cctgtgtgtg gctccaatgg ggagagctac cagaatgagt gttacctgcg acaggctgca 360  
tgcaaacagc agagtgagat acttgtggtg tcagaaggat catgtgccac agatgcagga 420  
tcaggatctg gagatggagt ccatgaaggc tctggagaaa ctagtcaaaa ggagacatcc 480

acctgtgata ttgcccagtt tgggtgcagaa tgtgacgaag atgccgagga tgtctgggtgt 540  
 gtgtgtaata ttgactgttc tcaaaccaac ttcaatcccc tctgcgcttc tgatgggaaa 600  
 tcttatgata atgcatgcca aatcaaagaa gcatcgtgtc agaaacagga gaaaattgaa 660  
 gtcattgtctt tgggtcgatg tcaagataac acaactacaa ctactaagtc tgaagatggg 720  
 cattatgcaa gaacagatta tgcagagaat gctaacaat tagaagaaag tgccagagaa 780  
 caccacatac cttgtccgga acattacaat ggcttctgca tgcattgggaa gtgtgagcat 840  
  
 tctatcaata tgcaggagcc atcttgcagg tgtgatgctg gttatactgg acaacactgt 900  
 gaaaaaaagg actacagtgt tctatacgtt gtccccggtc ctgtacgatt tcagtatgtc 960  
 ttaatcgcag ctgtgattgg aacaattcag attgctgtca tctgtgtggt ggctcctctgc 1020  
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<210> 27  
 <211> 1721  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (368) .. (1489)

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 cccgcgtctc cggcgcagct tctcagcggg cgaccctctc gctccggggc tgagccagtc 180  
 cctggatggt gctgaaactc tcgagatcat gcgcggggtt ggctgctgct tccccgccgg 240  
 gtgccactgc caccgccgcc gcctctgctg ccgccgtccg cgggatgctc agtagccgcg 300  
 tgccccggccc ccgcgatact gtgttcctcg gaagccggtt gctgctgcag agttgcacga 360

actagtc	atg	gtg	ctg	tgg	gag	tcc	ccg	cgg	cag	tgc	agc	agc	tgg	aca	409	
	Met	Val	Leu	Trp	Glu	Ser	Pro	Arg	Gln	Cys	Ser	Ser	Trp	Thr		
	1				5					10						
ctt	tgc	gag	ggc	ttt	tgc	tgg	ctg	ctg	ctg	ctg	ccc	gtc	atg	cta	ctc	457
Leu	Cys	Glu	Gly	Phe	Cys	Trp	Leu	Leu	Leu	Leu	Pro	Val	Met	Leu	Leu	
15					20					25					30	
atc	gta	gcc	cgc	ccg	gtg	aag	ctc	gct	gct	ttc	cct	acc	tcc	tta	agt	505
Ile	Val	Ala	Arg	Pro	Val	Lys	Leu	Ala	Ala	Phe	Pro	Thr	Ser	Leu	Ser	
				35					40					45		
gac	tgc	caa	acg	ccc	acc	ggc	tgg	aat	tgc	tct	ggc	tat	gat	gac	aga	553
Asp	Cys	Gln	Thr	Pro	Thr	Gly	Trp	Asn	Cys	Ser	Gly	Tyr	Asp	Asp	Arg	
			50					55					60			
gaa	aat	gat	ctc	ttc	ctc	tgt	gac	acc	aac	acc	tgt	aaa	ttt	gat	ggg	601
Glu	Asn	Asp	Leu	Phe	Leu	Cys	Asp	Thr	Asn	Thr	Cys	Lys	Phe	Asp	Gly	
		65					70					75				
gaa	tgt	tta	aga	att	gga	gac	act	gtg	act	tgc	gtc	tgt	cag	ttc	aag	649
Glu	Cys	Leu	Arg	Ile	Gly	Asp	Thr	Val	Thr	Cys	Val	Cys	Gln	Phe	Lys	
	80					85					90					
tgc	aac	aat	gac	tat	gtg	cct	gtg	tgt	ggc	tcc	aat	ggg	gag	agc	tac	697
Cys	Asn	Asn	Asp	Tyr	Val	Pro	Val	Cys	Gly	Ser	Asn	Gly	Glu	Ser	Tyr	
95					100					105					110	
cag	aat	gag	tgt	tac	ctg	cga	cag	gct	gca	tgc	aaa	cag	cag	agt	gag	745
Gln	Asn	Glu	Cys	Tyr	Leu	Arg	Gln	Ala	Ala	Cys	Lys	Gln	Gln	Ser	Glu	
				115					120					125		
ata	ctt	gtg	gtg	tca	gaa	gga	tca	tgt	gcc	aca	gat	gca	gga	tca	gga	793
Ile	Leu	Val	Val	Ser	Glu	Gly	Ser	Cys	Ala	Thr	Asp	Ala	Gly	Ser	Gly	
			130					135					140			
tct	gga	gat	gga	gtc	cat	gaa	ggc	tct	gga	gaa	act	agt	caa	aag	gag	841
Ser	Gly	Asp	Gly	Val	His	Glu	Gly	Ser	Gly	Glu	Thr	Ser	Gln	Lys	Glu	
		145					150					155				
aca	tcc	acc	tgt	gat	att	tgc	cag	ttt	ggc	gca	gaa	tgt	gac	gaa	gat	889
Thr	Ser	Thr	Cys	Asp	Ile	Cys	Gln	Phe	Gly	Ala	Glu	Cys	Asp	Glu	Asp	
	160					165					170					
gcc	gag	gat	gtc	tgg	tgt	gtg	tgt	aat	att	gac	tgt	tct	caa	acc	aac	937

Ala 175	Glu	Asp	Val	Trp	Cys 180	Val	Cys	Asn	Ile	Asp 185	Cys	Ser	Gln	Thr	Asn 190	
ttc	aat	ccc	ctc	tgc	gct	tct	gat	ggg	aaa	tct	tat	gat	aat	gca	tgc	985
Phe	Asn	Pro	Leu	Cys 195	Ala	Ser	Asp	Gly	Lys 200	Ser	Tyr	Asp	Asn	Ala 205	Cys	
caa	atc	aaa	gaa	gca	tcg	tgt	cag	aaa	cag	gag	aaa	att	gaa	gtc	atg	1033
Gln	Ile	Lys	Glu	Ala 210	Ser	Cys	Gln	Lys 215	Gln	Glu	Lys	Ile	Glu 220	Val	Met	
tct	ttg	ggg	cga	tgt	caa	gat	aac	aca	act	aca	act	act	aag	tct	gaa	1081
Ser	Leu	Gly 225	Arg	Cys	Gln	Asp	Asn 230	Thr	Thr	Thr	Thr	Thr	Lys 235	Ser	Glu	
gat	ggg	cat	tat	gca	aga	aca	gat	tat	gca	gag	aat	gct	aac	aaa	tta	1129
Asp	Gly 240	His	Tyr	Ala	Arg	Thr 245	Asp	Tyr	Ala	Glu	Asn 250	Ala	Asn	Lys	Leu	
gaa	gaa	agt	gcc	aga	gaa	cac	cac	ata	cct	tgt	ccg	gaa	cat	tac	aat	1177
Glu 255	Glu	Ser	Ala	Arg	Glu 260	His	His	Ile	Pro	Cys 265	Pro	Glu	His	Tyr	Asn 270	
ggc	ttc	tgc	atg	cat	ggg	aag	tgt	gag	cat	tct	atc	aat	atg	cag	gag	1225
Gly	Phe	Cys	Met	His 275	Gly	Lys	Cys	Glu	His 280	Ser	Ile	Asn	Met	Gln 285	Glu	
cca	tct	tgc	agg	tgt	gat	gct	ggg	tat	act	gga	caa	cac	tgt	gaa	aaa	1273
Pro	Ser	Cys	Arg 290	Cys	Asp	Ala	Gly	Tyr 295	Thr	Gly	Gln	His	Cys 300	Glu	Lys	
aag	gac	tac	agt	gtt	cta	tac	gtt	gtt	ccc	ggg	cct	gta	cga	ttt	cag	1321
Lys	Asp	Tyr 305	Ser	Val	Leu	Tyr	Val 310	Val	Pro	Gly	Pro	Val 315	Arg	Phe	Gln	
tat	gtc	tta	atc	gca	gct	gtg	att	gga	aca	att	cag	att	gct	gtc	atc	1369
Tyr	Val 320	Leu	Ile	Ala	Ala	Val 325	Ile	Gly	Thr	Ile	Gln 330	Ile	Ala	Val	Ile	
tgt	gtg	gtg	gtc	ctc	tgc	atc	aca	agg	aaa	tgc	ccc	aga	agc	aac	aga	1417
Cys 335	Val	Val	Val	Leu	Cys 340	Ile	Thr	Arg	Lys	Cys 345	Pro	Arg	Ser	Asn	Arg 350	
att	cac	aga	cag	aag	caa	aat	aca	ggg	cac	tac	agt	tca	gac	aat	aca	1465
Ile	His	Arg	Gln	Lys 355	Gln	Asn	Thr	Gly	His 360	Tyr	Ser	Ser	Asp	Asn 365	Thr	

aca aga gcg tcc acg agg tta atc taaagggagc atgtttcaca gtggctggac 1519  
 Thr Arg Ala Ser Thr Arg Leu Ile  
 370

taccgagagc ttggactaca caatacagta ttatagacaa aagaataaga caagagatct 1579  
 acacatgttg ccttgcattt gtggtaatct acaccaatga aaacatgtac tacagctata 1639  
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<210> 28  
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 <212> PRT  
 <213> Homo sapiens

<400> 28  
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           20                  25                  30  
 Ile Thr Glu Gly Val Gly Glu Leu Ser Val Ile Asp Pro Glu Val Ala  
       35                  40                  45  
 Gln Lys Ala Cys Gln Glu Val Leu Glu Lys Val Lys Leu Leu His Gly  
       50                  55                  60  
 Gly Val Ala Val Ser Ser Arg Gly Thr Pro Leu Glu Leu Val Asn Gly  
   65                  70                  75                  80  
 Asp Gly Val Asp Ser Glu Ile Arg Cys Leu Asp Asp Pro Pro Ala Gln  
           85                  90                  95  
 Ile Arg Glu Glu Glu Asp Glu Met Gly Ala Ala Val Ala Ser Gly Thr  
           100                  105                  110  
 Ala Lys Gly Ala Arg Arg Arg Arg Gln Asn Asn Ser Ala Lys Gln Ser  
       115                  120                  125  
 Trp Leu Leu Arg Leu Phe Glu Ser Lys Leu Phe Asp Ile Ser Met Ala  
       130                  135                  140

Ile	Ser	Tyr	Leu	Tyr	Asn	Ser	Lys	Glu	Pro	Gly	Val	Gln	Ala	Tyr	Ile	145	150	155	160
Gly	Asn	Arg	Leu	Phe	Cys	Phe	Arg	Asn	Glu	Asp	Val	Asp	Phe	Tyr	Leu	165	170	175	
Pro	Gln	Leu	Leu	Asn	Met	Tyr	Ile	His	Met	Asp	Glu	Asp	Val	Gly	Asp	180	185	190	
Ala	Ile	Lys	Pro	Tyr	Ile	Val	His	Arg	Cys	Arg	Gln	Ser	Ile	Asn	Phe	195	200	205	
Ser	Leu	Gln	Cys	Ala	Leu	Leu	Leu	Gly	Ala	Tyr	Ser	Ser	Asp	Met	His	210	215	220	
Ile	Ser	Thr	Gln	Arg	His	Ser	Arg	Gly	Thr	Lys	Leu	Arg	Lys	Leu	Ile	225	230	235	240
Leu	Ser	Asp	Glu	Leu	Lys	Pro	Ala	His	Arg	Lys	Arg	Glu	Leu	Pro	Ser	245	250	255	
Leu	Ser	Pro	Ala	Pro	Asp	Thr	Gly	Leu	Ser	Pro	Ser	Lys	Arg	Thr	His	260	265	270	
Gln	Arg	Ser	Lys	Ser	Asp	Ala	Thr	Ala	Ser	Ile	Ser	Leu	Ser	Ser	Asn	275	280	285	
Leu	Lys	Arg	Thr	Ala	Ser	Asn	Pro	Lys	Val	Glu	Asn	Glu	Asp	Glu	Glu	290	295	300	
Leu	Ser	Ser	Ser	Thr	Glu	Ser	Ile	Asp	Asn	Ser	Phe	Ser	Ser	Pro	Val	305	310	315	320
Arg	Leu	Ala	Pro	Glu	Arg	Glu	Phe	Ile	Lys	Ser	Leu	Met	Ala	Ile	Gly	325	330	335	
Lys	Arg	Leu	Ala	Thr	Leu	Pro	Thr	Lys	Glu	Gln	Lys	Thr	Gln	Arg	Leu	340	345	350	
Ile	Ser	Glu	Leu	Ser	Leu	Leu	Asn	His	Lys	Leu	Pro	Ala	Arg	Val	Trp	355	360	365	
Leu	Pro	Thr	Ala	Gly	Phe	Asp	His	His	Val	Val	Arg	Val	Pro	His	Thr	370	375	380	

Gln Ala Val Val Leu Asn Ser Lys Asp Lys Ala Pro Tyr Leu Ile Tyr  
 385 390 395 400

Val Glu Val Leu Glu Cys Glu Asn Phe Asp Thr Thr Ser Val Pro Ala  
 405 410 415

Arg Ile Pro Glu Asn Arg Ile Arg Ser Thr Arg Ser Val Glu Asn Leu  
 420 425 430

Pro Glu Cys Gly Ile Thr His Glu Gln Arg Ala Gly Ser Phe Ser Thr  
 435 440 445

Val Pro Asn Tyr Asp Asn Asp Asp Glu Ala Trp Ser Val Asp Asp Ile  
 450 455 460

Gly Glu Leu Gln Val Glu Leu Pro Glu Val His Thr Asn Ser Cys Asp  
 465 470 475 480

Asn Ile Ser Gln Phe Ser Val Asp Ser Ile Thr Ser Gln Glu Ser Lys  
 485 490 495

Glu Pro Val Phe Ile Ala Ala Gly Asp Ile Arg Arg Arg Leu Ser Glu  
 500 505 510

Gln Leu Ala His Thr Pro Thr Ala Phe Lys Arg Asp Pro Glu Asp Pro  
 515 520 525

Ser Ala Val Ala Leu Lys Glu Pro Trp Gln Glu Lys Val Arg Arg Ile  
 530 535 540

Arg Glu Gly Ser Pro Tyr Gly His Leu Pro Asn Trp Arg Leu Leu Ser  
 545 550 555 560

Val Ile Val Lys Cys Gly Asp Asp Leu Arg Gln Glu Leu Leu Ala Phe  
 565 570 575

Gln Val Leu Lys Gln Leu Gln Ser Ile Trp Glu Gln Glu Arg Val Pro  
 580 585 590

Leu Trp Ile Lys Pro Ile Gln Asp Ser Cys Glu Ile Thr Thr Asp Ser  
 595 600 605

Gly Met Ile Glu Pro Val Val Asn Ala Val Ser Ile His Gln Val Lys  
 610 615 620

Lys	Gln	Ser	Gln	Leu	Ser	Leu	Leu	Asp	Tyr	Phe	Leu	Gln	Glu	His	Gly	625	630	635	640
Ser	Tyr	Thr	Thr	Glu	Ala	Phe	Leu	Ser	Ala	Gln	Arg	Asn	Phe	Val	Gln	645	650	655	
Ser	Cys	Ala	Gly	Tyr	Cys	Leu	Val	Cys	Tyr	Leu	Leu	Gln	Val	Lys	Asp	660	665	670	
Arg	His	Asn	Gly	Asn	Ile	Leu	Leu	Asp	Ala	Glu	Gly	His	Ile	Ile	His	675	680	685	
Ile	Asp	Phe	Gly	Phe	Ile	Leu	Ser	Ser	Ser	Pro	Arg	Asn	Leu	Gly	Phe	690	695	700	
Glu	Thr	Ser	Ala	Phe	Lys	Leu	Thr	Thr	Glu	Phe	Val	Asp	Val	Met	Gly	705	710	715	720
Gly	Leu	Asp	Gly	Asp	Met	Phe	Asn	Tyr	Tyr	Lys	Met	Leu	Met	Leu	Gln	725	730	735	
Gly	Leu	Ile	Ala	Ala	Arg	Lys	His	Met	Asp	Lys	Val	Val	Gln	Ile	Val	740	745	750	
Glu	Ile	Met	Gln	Gln	Gly	Ser	Gln	Leu	Pro	Cys	Phe	His	Gly	Ser	Ser	755	760	765	
Thr	Ile	Arg	Asn	Leu	Lys	Glu	Arg	Phe	His	Met	Ser	Met	Thr	Glu	Glu	770	775	780	
Gln	Leu	Gln	Leu	Leu	Val	Glu	Gln	Met	Val	Asp	Gly	Ser	Met	Arg	Ser	785	790	795	800
Ile	Thr	Thr	Lys	Leu	Tyr	Asp	Gly	Phe	Gln	Tyr	Leu	Thr	Asn	Gly	Ile	805	810	815	

Met

<210> 29

<211> 2451

<212> DNA

<213> Homo sapiens

<400> 29

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Asn Gly Asp Gly Val Asp Ser Glu Ile Arg Cys Leu Asp Asp Pro Pro

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85

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 Ser Glu Ile Arg Cys Leu Asp Asp Pro Pro Ala Gln Ile Arg Glu Glu  
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Pro Tyr Gly His Leu Pro Asn Trp Arg Leu Leu Ser Val Ile Val Lys  
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Cys Gly Asp Asp Leu Arg Gln Glu Leu Leu Ala Phe Gln Val Leu Lys  
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Gln Leu Gln Ser Ile Trp Glu Gln Glu Arg Val Pro Leu Trp Ile Lys  
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Pro Cys Leu Ala Asp Asn Ile Thr Tyr Asp Ile Arg Lys Thr Cys Leu  
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<212> DNA

<213> Homo sapiens

<400> 35

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<213> Homo sapiens

<400> 37

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Leu	Thr	Glu	Leu	Glu	Leu	Gly	Glu	Ser	Thr	Thr	Gly	Val	Arg	Gln	Val			
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Pro	Gly	Leu	His	Asn	Gly	Thr	Lys	Ala	Phe	Leu	Phe	Gln	Asp	Thr	Pro			
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His	Leu	Asn	Ser	Gly	Val	Ile	Leu	Ser	Ile	His	His	Leu	Asp	His	Arg			
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Tyr	Leu	Glu	Leu	Glu	Ser	Ser	Gly	His	Arg	Asn	Glu	Val	Arg	Leu	His			
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Tyr	Arg	Ser	Gly	Ser	His	Arg	Pro	His	Thr	Glu	Val	Phe	Pro	Tyr	Ile			
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Leu	Ala	Asp	Asp	Lys	Trp	His	Lys	Leu	Ser	Leu	Ala	Ile	Ser	Ala	Ser			
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His	Leu	Ile	Leu	His	Ile	Asp	Cys	Asn	Lys	Ile	Tyr	Glu	Arg	Val	Val			
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Ile	Met	Glu	Leu	Gln	Asp	Ile	Leu	Ala	Lys	Thr	Ser	Ala	Lys	Leu	Ser			

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		275					280					285					
Asp	Gly	Cys	Lys	Asn	Cys	Thr	Cys	Leu	Asn	Gly	Thr	Ile	Gln	Cys	Glu		
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Tyr	Val	Asp	Gly	Lys	Cys	Cys	Lys	Glu	Cys	Lys	Ser	Ile	Cys	Gln	Phe		
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Gln	Gly	Arg	Thr	Tyr	Phe	Glu	Gly	Glu	Arg	Asn	Thr	Val	Tyr	Ser	Ser		
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Val	Glu	Ser	Ser	Gly	Cys	Pro	Ala	Leu	Asp	Cys	Pro	Glu	Ser	His	Gln		
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Gln	Cys	Arg	Cys	Leu	Gln	Gly	Glu	Val	Asp	Cys	Trp	Pro	Leu	Pro	Cys
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740 745 750

Pro Arg Cys Val Thr Asp Pro Cys Gln Ala Asp Thr Ile Arg Asn Asp  
755 760 765

Ile Thr Lys Thr Cys Leu Asp Glu Met Asn Val Val Arg Phe Thr Gly  
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<210> 38

<211> 2448

<212> DNA

<213> Homo sapiens

<400> 38

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Ser	Gly	His	Arg	Asn	Glu	Val	Arg	Leu	His	Tyr	Arg	Ser	Gly	Ser	His	
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cgc	cct	cac	aca	gaa	gtg	ttt	cct	tac	att	ttg	gct	gat	gac	aag	tgg	546
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Asp	Cys	Asn	Lys	Ile	Tyr	Glu	Arg	Val	Val	Glu	Lys	Pro	Ser	Thr	Asp	
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Leu	Pro	Leu	Gly	Thr	Thr	Phe	Trp	Leu	Gly	Gln	Arg	Asn	Asn	Ala	His	
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Cys	Lys	Glu	Cys	Lys	Ser	Ile	Cys	Gln	Phe	Gln	Gly	Arg	Thr	Tyr	Phe	
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Gly Tyr Ile Arg Ile Asp Asp Tyr Ser Cys Thr Glu His Asp Glu Cys	
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Cys Arg Asp Gly Tyr His Asp Asn Gly Met Phe Ser Pro Ser Gly Glu	
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Ser Cys Glu Asp Ile Asp Glu Cys Gly Thr Gly Arg His Ser Cys Ala	
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Asn Asp Thr Ile Cys Phe Asn Leu Asp Gly Gly Tyr Asp Cys Arg Cys	

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Phe Ser Ile Leu Pro Glu Asn Glu Cys Cys Pro Arg Cys Val Thr Asp						Phe Ser Ile Leu Pro Glu Asn Glu Cys Cys Pro Arg Cys Val Thr Asp													
	745						750						755						
cct tgc cag gct gac acc atc cgc aat gac atc acc aag act tgc ctg						cct tgc cag gct gac acc atc cgc aat gac atc acc aag act tgc ctg						2418							
Pro Cys Gln Ala Asp Thr Ile Arg Asn Asp Ile Thr Lys Thr Cys Leu						Pro Cys Gln Ala Asp Thr Ile Arg Asn Asp Ile Thr Lys Thr Cys Leu													
	760						765						770						
gac gaa atg aat gtg gtt cgc ttc acc ggg tcc tct tgg atc aaa cat						gac gaa atg aat gtg gtt cgc ttc acc ggg tcc tct tgg atc aaa cat						2466							
Asp Glu Met Asn Val Val Arg Phe Thr Gly Ser Ser Trp Ile Lys His						Asp Glu Met Asn Val Val Arg Phe Thr Gly Ser Ser Trp Ile Lys His													
	775						780						785						
ggc act gag tgt act ctc tgc cag tgc aag aat ggc cac atc tgt tgc						ggc act gag tgt act ctc tgc cag tgc aag aat ggc cac atc tgt tgc						2514							
Gly Thr Glu Cys Thr Leu Cys Gln Cys Lys Asn Gly His Ile Cys Cys						Gly Thr Glu Cys Thr Leu Cys Gln Cys Lys Asn Gly His Ile Cys Cys													
	795						800						805						

tca gtg gat cca cag tgc ctt cag gaa ctg tgaagttaac tgtctcatgg 2564  
 Ser Val Asp Pro Gln Cys Leu Gln Glu Leu  
           810                                  815

gagattttctg ttaaaagaat gttctttcat taaaagacca aaaagaagtt aaaacttaaa 2624  
 ttgggtgatt tgtgggcagc taaatgcagc tttgttaata gctgagtga ctttcaatta 2684  
 tgaaatttgt ggagcttgac aaaatcacaa aaggaaaatt actggggcaa aattagacct 2744  
 caagtctgcc tctactgtgt ctcacatcac catgtagaag aatgggcgta cagtatatac 2804  
 cgtgacatcc tgaaccctgg atagaaagcc tgagcccatt ggatctgtga aagcctctag 2864  
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 gataaaaata atgcacaggc atggttactt aatattttct aacaggaaaa gtcaccccta 3104  
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 <212> PRT  
 <213> Homo sapiens

<400> 40  
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 Leu Glu Glu Ser Trp Glu His Ser Lys Glu Val Ser Glu Ala Glu Pro  
           20                  25                  30  
 Gly Gly Gly Ser Ser Gly Asp Ser Gly Pro Pro Glu Glu Ser Gly Gln  
           35                  40                  45  
 Glu Met Met Glu Glu Lys Glu Glu Ile Arg Lys Ser Lys Ser Val Ile  
   50                  55                  60



Val 65	Pro	Ser	Gly	Ala	Pro 70	Lys	Lys	Glu	His	Val 75	Asn	Val	Val	Phe	Ile 80
Gly	His	Val	Asp	Ala 85	Gly	Lys	Ser	Thr	Ile 90	Gly	Gly	Gln	Ile	Met	Phe 95
Leu	Thr	Gly	Met 100	Ala	Asp	Lys	Arg	Thr 105	Leu	Glu	Lys	Tyr	Glu 110	Arg	Glu
Ala	Glu	Glu	Lys	Asn	Arg	Glu	Thr 120	Trp	Tyr	Leu	Ser	Trp 125	Ala	Leu	Asp
Thr	Asn 130	Gln	Glu	Glu	Arg	Asp 135	Lys	Gly	Lys	Thr	Val 140	Glu	Val	Gly	Arg
Ala 145	Tyr	Phe	Glu	Thr	Glu 150	Arg	Lys	His	Phe	Thr 155	Ile	Leu	Asp	Ala	Pro 160
Gly	His	Lys	Ser	Phe 165	Val	Pro	Asn	Met	Ile 170	Gly	Gly	Ala	Ser	Gln	Ala 175
Asp	Leu	Ala	Val 180	Leu	Val	Ile	Ser	Ala 185	Arg	Lys	Gly	Glu	Phe 190	Glu	Thr
Gly	Phe 195	Glu	Lys	Gly	Gly	Gln	Thr 200	Arg	Glu	His	Ala	Met 205	Phe	Gly	Lys
Thr 210	Ala	Gly	Val	Lys	His	Leu 215	Ile	Val	Leu	Ile	Asn 220	Lys	Met	Asp	Asp
Pro 225	Thr	Val	Asn	Trp	Gly 230	Ile	Glu	Arg	Tyr	Glu 235	Glu	Cys	Lys	Glu	Lys 240
Leu	Val	Pro	Phe	Leu 245	Lys	Lys	Val	Gly	Phe 250	Ser	Pro	Lys	Lys	Asp 255	Ile
His	Phe	Met	Pro 260	Cys	Ser	Gly	Leu	Thr 265	Gly	Ala	Asn	Ile	Lys 270	Glu	Gln
Ser	Asp	Phe 275	Cys	Pro	Trp	Tyr	Thr 280	Gly	Leu	Pro	Phe	Ile 285	Pro	Tyr	Leu
Asn 290	Asn	Leu	Pro	Asn	Phe	Asn 295	Arg	Ser	Ile	Asp	Gly 300	Pro	Ile	Arg	Leu
Pro	Ile	Val	Asp	Lys	Tyr	Lys	Asp	Met	Gly	Thr	Val	Val	Leu	Gly	Lys

305		310		315		320									
Leu	Glu	Ser	Gly	Ser	Ile	Phe	Lys	Gly	Gln	Gln	Leu	Val	Met	Met	Pro
				325					330					335	
Asn	Lys	His	Asn	Val	Glu	Val	Leu	Gly	Ile	Leu	Ser	Asp	Asp	Thr	Glu
			340					345					350		
Thr	Asp	Phe	Val	Ala	Pro	Gly	Glu	Asn	Leu	Lys	Ile	Arg	Leu	Lys	Gly
		355					360					365			
Ile	Glu	Glu	Glu	Glu	Ile	Leu	Pro	Glu	Phe	Ile	Leu	Cys	Asp	Pro	Ser
	370					375					380				
Asn	Leu	Cys	His	Ser	Gly	Arg	Thr	Phe	Asp	Val	Gln	Ile	Val	Ile	Ile
385					390					395					400
Glu	His	Lys	Ser	Ile	Ile	Cys	Pro	Gly	Tyr	Asn	Ala	Val	Leu	His	Ile
				405					410					415	
His	Thr	Cys	Ile	Glu	Glu	Val	Glu	Ile	Thr	Ala	Leu	Ile	Ser	Leu	Val
			420					425					430		
Asp	Lys	Lys	Ser	Gly	Glu	Lys	Ser	Lys	Thr	Arg	Pro	Arg	Phe	Val	Lys
		435					440					445			
Gln	Asp	Gln	Val	Cys	Ile	Ala	Arg	Leu	Arg	Thr	Ala	Gly	Thr	Ile	Cys
	450					455					460				
Leu	Glu	Thr	Phe	Lys	Asp	Phe	Pro	Gln	Met	Gly	Arg	Phe	Thr	Leu	Arg
465					470					475					480
Asp	Glu	Gly	Lys	Thr	Ile	Ala	Ile	Gly	Lys	Val	Leu	Lys	Leu	Val	Pro
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Glu	Lys	Asp													

<210> 41

<211> 1497

<212> DNA

<213> Homo sapiens

<400> 41

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 gggccccag aagaaagtgg ccaggaaatg atggaggaaa aagaggaaat aagaaaatcc 180  
 aaatctgtga tcgtaccctc aggtgcacct aagaaagaac acgtaaatgt agtattcatt 240  
 ggccatgtag acgctggcaa gtcaaccatc ggaggacaga taatgttttt gactggaatg 300  
 gctgacaaaa gaacactgga gaaatatgaa agagaagctg aggaaaaaaa cagagaaacc 360  
 tggatatttgt cctgggcctt agatacaaat caggaggaac gagacaaggg taaaacagtc 420  
 gaagtgggtc gtgcctattt tgaaacagaa aggaacatt tcacaatttt agatgccctt 480  
 ggccacaaga gttttgtccc aaatatgatt ggtggtgctt ctcaagctga tttggctgtg 540  
 ctggtcatct ctgccaggaa aggagagttt gaaactggat ttgaaaaagg tggacagaca 600  
 agagaacatg cgatgtttgg caaacggca ggagtaaac atttaatagt gcttattaat 660  
 aagatggatg atcccacagt aaattggggc atcgagagat atgaagaatg taaagaaaaa 720  
 ctggtgccct ttttgaaaaa agtaggcttt agtccaaaaa aggacattca ctttatgccc 780  
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 ggattaccat ttattccgta tttgaataac ttgccaaact tcaacagatc aattgatgga 900  
 ccaataagac tgccaattgt ggataagtac aaagatatgg gcactgtggt cctgggaaag 960  
 ctggaatccg ggtccatttt taaaggccag cagctcgtga tgatgccaaa caagcacaat 1020  
 gtagaagttc ttggaatact ttctgatgat actgaaactg attttgtagc cccaggtgaa 1080  
 aacctcaaaa tcagactgaa ggaattgaa gaagaagaga ttcttccaga attcatactt 1140  
 tgtgatccta gtaacctctg ccattctgga cgcacgtttg atgttcagat agtgattatt 1200  
 gagcacaaat ccatcatctg cccaggttat aatgcggtgc tgcacattca tacttgtatt 1260  
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 aagacacgac cccgcttcgt gaaacaagat caagtatgca ttgctcgttt aaggacagca 1380  
 ggaaccatct gcctcgagac gttcaaagat tttcctcaga tgggtcgttt tactttaaga 1440

gatgagggta agaccattgc aattggaaaa gttctgaaat tgggtcccaga gaaggac 1497

<210> 42

<211> 2057

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (144)..(1640)

<400> 42

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aaaggatggg acgggggggca cctgtggaac cttcccgaga ggaaccgtta gtgtcgcttg 120

aaggttccaa ttcagccggtt acc atg gaa ctt tca gaa cct gtt gta gaa aat 173

Met Glu Leu Ser Glu Pro Val Val Glu Asn

1

5

10

gga gag gtg gaa atg gcc cta gaa gaa tca tgg gag cac agt aaa gaa 221

Gly Glu Val Glu Met Ala Leu Glu Glu Ser Trp Glu His Ser Lys Glu

15

20

25

gta agt gaa gcc gag cct ggg ggt ggt tcc tcg gga gat tca ggg ccc 269

Val Ser Glu Ala Glu Pro Gly Gly Gly Ser Ser Gly Asp Ser Gly Pro

30

35

40

cca gaa gaa agt ggc cag gaa atg atg gag gaa aaa gag gaa ata aga 317

Pro Glu Glu Ser Gly Gln Glu Met Met Glu Glu Lys Glu Glu Ile Arg

45

50

55

aaa tcc aaa tct gtg atc gta ccc tca ggt gca cct aag aaa gaa cac 365

Lys Ser Lys Ser Val Ile Val Pro Ser Gly Ala Pro Lys Lys Glu His

60

65

70

gta aat gta gta ttc att ggc cat gta gac gct ggc aag tca acc atc 413

Val Asn Val Val Phe Ile Gly His Val Asp Ala Gly Lys Ser Thr Ile

75

80

85

90

gga gga cag ata atg ttt ttg act gga atg gct gac aaa aga aca ctg 461

Gly Gly Gln Ile Met Phe Leu Thr Gly Met Ala Asp Lys Arg Thr Leu

95						100						105						
gag	aaa	tat	gaa	aga	gaa	gct	gag	gaa	aaa	aac	aga	gaa	acc	tgg	tat	509		
Glu	Lys	Tyr	Glu	Arg	Glu	Ala	Glu	Glu	Lys	Asn	Arg	Glu	Thr	Trp	Tyr			
			110						115			120						
ttg	tcc	tgg	gcc	tta	gat	aca	aat	cag	gag	gaa	cga	gac	aag	ggg	aaa	557		
Leu	Ser	Trp	Ala	Leu	Asp	Thr	Asn	Gln	Glu	Glu	Arg	Asp	Lys	Gly	Lys			
			125						130			135						
aca	gtc	gaa	gtg	ggg	cgt	gcc	tat	ttt	gaa	aca	gaa	agg	aaa	cat	ttc	605		
Thr	Val	Glu	Val	Gly	Arg	Ala	Tyr	Phe	Glu	Thr	Glu	Arg	Lys	His	Phe			
			140						145			150						
aca	att	tta	gat	gcc	cct	ggc	cac	aag	agt	ttt	gtc	cca	aat	atg	att	653		
Thr	Ile	Leu	Asp	Ala	Pro	Gly	His	Lys	Ser	Phe	Val	Pro	Asn	Met	Ile			
			155						160			165			170			
ggg	ggg	gct	tct	caa	gct	gat	ttg	gct	gtg	ctg	gtc	atc	tct	gcc	agg	701		
Gly	Gly	Ala	Ser	Gln	Ala	Asp	Leu	Ala	Val	Leu	Val	Ile	Ser	Ala	Arg			
			175						180			185						
aaa	gga	gag	ttt	gaa	act	gga	ttt	gaa	aaa	ggg	gga	cag	aca	aga	gaa	749		
Lys	Gly	Glu	Phe	Glu	Thr	Gly	Phe	Glu	Lys	Gly	Gly	Gln	Thr	Arg	Glu			
			190						195			200						
cat	gcg	atg	ttt	ggc	aaa	acg	gca	gga	gta	aaa	cat	tta	ata	gtg	ctt	797		
His	Ala	Met	Phe	Gly	Lys	Thr	Ala	Gly	Val	Lys	His	Leu	Ile	Val	Leu			
			205						210			215						
att	aat	aag	atg	gat	gat	ccc	aca	gta	aat	tgg	ggc	atc	gag	aga	tat	845		
Ile	Asn	Lys	Met	Asp	Asp	Pro	Thr	Val	Asn	Trp	Gly	Ile	Glu	Arg	Tyr			
			220						225			230						
gaa	gaa	tgt	aaa	gaa	aaa	ctg	gtg	ccc	ttt	ttg	aaa	aaa	gta	ggc	ttt	893		
Glu	Glu	Cys	Lys	Glu	Lys	Leu	Val	Pro	Phe	Leu	Lys	Lys	Val	Gly	Phe			
			235						240			245			250			
agt	cca	aaa	aag	gac	att	cac	ttt	atg	ccc	tgc	tca	gga	ctg	acc	gga	941		
Ser	Pro	Lys	Lys	Asp	Ile	His	Phe	Met	Pro	Cys	Ser	Gly	Leu	Thr	Gly			
			255						260			265						
gca	aat	att	aaa	gag	cag	tca	gat	ttc	tgc	cct	tgg	tac	act	gga	tta	989		
Ala	Asn	Ile	Lys	Glu	Gln	Ser	Asp	Phe	Cys	Pro	Trp	Tyr	Thr	Gly	Leu			
			270						275			280						

cca	ttt	att	ccg	tat	ttg	aat	aac	ttg	cca	aac	ttc	aac	aga	tca	att	1037
Pro	Phe	Ile	Pro	Tyr	Leu	Asn	Asn	Leu	Pro	Asn	Phe	Asn	Arg	Ser	Ile	
		285					290					295				
gat	gga	cca	ata	aga	ctg	cca	att	gtg	gat	aag	tac	aaa	gat	atg	ggc	1085
Asp	Gly	Pro	Ile	Arg	Leu	Pro	Ile	Val	Asp	Lys	Tyr	Lys	Asp	Met	Gly	
	300					305					310					
act	gtg	gtc	ctg	gga	aag	ctg	gaa	tcc	ggg	tcc	att	ttt	aaa	ggc	cag	1133
Thr	Val	Val	Leu	Gly	Lys	Leu	Glu	Ser	Gly	Ser	Ile	Phe	Lys	Gly	Gln	
315					320					325					330	
cag	ctc	gtg	atg	atg	cca	aac	aag	cac	aat	gta	gaa	ggt	ctt	gga	ata	1181
Gln	Leu	Val	Met	Met	Pro	Asn	Lys	His	Asn	Val	Glu	Val	Leu	Gly	Ile	
				335					340					345		
ctt	tct	gat	gat	act	gaa	act	gat	ttt	gta	gcc	cca	ggt	gaa	aac	ctc	1229
Leu	Ser	Asp	Asp	Thr	Glu	Thr	Asp	Phe	Val	Ala	Pro	Gly	Glu	Asn	Leu	
			350					355					360			
aaa	atc	aga	ctg	aag	gga	att	gaa	gaa	gaa	gag	att	ctt	cca	gaa	ttc	1277
Lys	Ile	Arg	Leu	Lys	Gly	Ile	Glu	Glu	Glu	Glu	Ile	Leu	Pro	Glu	Phe	
		365					370					375				
ata	ctt	tgt	gat	cct	agt	aac	ctc	tgc	cat	tct	gga	cgc	acg	ttt	gat	1325
Ile	Leu	Cys	Asp	Pro	Ser	Asn	Leu	Cys	His	Ser	Gly	Arg	Thr	Phe	Asp	
	380					385					390					
gtt	cag	ata	gtg	att	att	gag	cac	aaa	tcc	atc	atc	tgc	cca	ggt	tat	1373
Val	Gln	Ile	Val	Ile	Ile	Glu	His	Lys	Ser	Ile	Ile	Cys	Pro	Gly	Tyr	
395					400					405					410	
aat	gcg	gtg	ctg	cac	att	cat	act	tgt	att	gag	gaa	ggt	gag	ata	aca	1421
Asn	Ala	Val	Leu	His	Ile	His	Thr	Cys	Ile	Glu	Glu	Val	Glu	Ile	Thr	
				415				420						425		
gcg	tta	atc	tcc	ttg	gta	gac	aaa	aaa	tca	ggg	gaa	aaa	agt	aag	aca	1469
Ala	Leu	Ile	Ser	Leu	Val	Asp	Lys	Lys	Ser	Gly	Glu	Lys	Ser	Lys	Thr	
			430					435					440			
cga	ccc	cgc	ttc	gtg	aaa	caa	gat	caa	gta	tgc	att	gct	cgt	tta	agg	1517
Arg	Pro	Arg	Phe	Val	Lys	Gln	Asp	Gln	Val	Cys	Ile	Ala	Arg	Leu	Arg	
		445					450					455				
aca	gca	gga	acc	atc	tgc	ctc	gag	acg	ttc	aaa	gat	ttt	cct	cag	atg	1565
Thr	Ala	Gly	Thr	Ile	Cys	Leu	Glu	Thr	Phe	Lys	Asp	Phe	Pro	Gln	Met	

460

465

470

ggt cgt ttt act tta aga gat gag ggt aag acc att gca att gga aaa 1613  
 Gly Arg Phe Thr Leu Arg Asp Glu Gly Lys Thr Ile Ala Ile Gly Lys  
 475 480 485 490

gtt ctg aaa ttg gtc cca gag aag gac taagcaattt tcttgatgcc 1660  
 Val Leu Lys Leu Val Pro Glu Lys Asp  
 495

tctgcaagat actgtgagga gaattgacag caaaagttca ccacctactc ttatttactg 1720  
 cccattgatt gacttttctt catatttttgc aaagagaaat ttcacagcaa aaattcatgt 1780  
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 gacgtaattg cctacagtaa taaaaaaata atgtacttta atttttcatt ttcttttagg 1960  
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 aaatgataac taacatgtga ataaaatact ccatttg 2057

&lt;210&gt; 43

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer P1

&lt;400&gt; 43

acaccaatcc agtagccagg cttg

24

&lt;210&gt; 44

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer P2

&lt;400&gt; 44

cactcgagaa tctgtgagac ctacatacat gacg

34

<210> 45

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<221> misc\_feature

<222> (2)..(20)

<223> Xaa can be any naturally occurring amino acid

<400> 45

Cys	Xaa	Glu	Cys	Gly	Lys	Ala	Phe	Xaa	Gln	Lys	Ser	Xaa	Leu	Xaa	Xaa
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His	Gln	Arg	Xaa	His
			20	

<210> 46

<211> 7

<212> PRT

<213> Bovine sp.

<400> 46

Val	Leu	Asn	Ile	Ser	Leu	Trp
1				5		

<210> 47

<211> 17

<212> PRT

<213> Bovine sp.

<400> 47

Thr	Leu	Met	Glu	Leu	Leu	Asn	Gln	Met	Asp	Gly	Phe	Asp	Thr	Leu	His
1				5					10					15	

Arg

<210> 48



<211> 14  
<212> PRT  
<213> Bovine sp.

<220>  
<221> misc\_feature  
<222> (11)..(13)  
<223> Xaa can be any naturally occurring amino acid

<400> 48  
Ala Val Ser Asp Phe Val Val Ser Glu Tyr Xaa Met Xaa Ala  
1 5 10

<210> 49  
<211> 9  
<212> PRT  
<213> Bovine sp.

<220>  
<221> misc\_feature  
<222> (9)..(9)  
<223> Xaa can be any naturally occurring amino acid

<400> 49  
Glu Val Asp Pro Leu Val Tyr Asn Xaa  
1 5

<210> 50  
<211> 11  
<212> PRT  
<213> Bovine sp.

<400> 50  
His Gly Glu Ile Asp Tyr Glu Ala Ile Val Lys  
1 5 10

<210> 51  
<211> 25  
<212> PRT  
<213> Bovine sp.

<220>  
<221> misc\_feature

<222> (3)..(23)

<223> Xaa can be any naturally occurring amino acid

<400> 51

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Ala	Gly	Met	Phe	Ala	Ile	Xaa	Ala	Asp
			20				25	

<210> 52

<211> 21

<212> PRT

<213> Bovine sp.

<220>

<221> misc\_feature

<222> (20)..(20)

<223> Xaa can be any naturally occurring amino acid

<400> 52

Met	Ile	Met	Ala	Thr	Asn	Arg	Pro	Asp	Thr	Leu	Asp	Pro	Ala	Leu	Leu
1				5					10					15	

Arg	Pro	Gly	Xaa	Leu
			20	

<210> 53

<211> 16

<212> PRT

<213> Bovine sp.

<400> 53

Ile	His	Ile	Asp	Leu	Pro	Asn	Glu	Gln	Ala	Arg	Leu	Asp	Ile	Leu	Lys
1				5					10					15	

<210> 54

<211> 11

<212> PRT

<213> Bovine sp.

<400> 54

Ala Thr Asn Gly Pro Arg Tyr Val Val Val Gly

1 5 10

<210> 55  
<211> 7  
<212> PRT  
<213> Bovine sp.

<400> 55  
Glu Ile Asp Gly Arg Leu Lys  
1 5

<210> 56  
<211> 14  
<212> PRT  
<213> Bovine sp.

<400> 56  
Ala Leu Gln Ser Val Gly Gln Ile Val Gly Glu Val Leu Lys  
1 5 10

<210> 57  
<211> 8  
<212> PRT  
<213> Bovine sp.

<400> 57  
Ile Leu Ala Gly Pro Ile Thr Lys  
1 5

<210> 58  
<211> 16  
<212> PRT  
<213> Bovine sp.

<220>  
<221> misc\_feature  
<222> (1)..(2)  
<223> Xaa can be any naturally occurring amino acid

<400> 58  
Xaa Xaa Val Ile Glu Leu Pro Leu Thr Asn Pro Glu Leu Phe Gln Gly  
1 5 10 15

<210> 59  
<211> 9  
<212> PRT  
<213> Bovine sp.

<400> 59  
Val Val Ser Ser Ser Leu Val Asp Lys  
1 5

<210> 60  
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<400> 63

Leu Val Pro Thr Arg

1 5

<210> 64

<211> 11

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<400> 64

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<211> 10

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<213> Bovine sp.

<400> 65

Ala Asn Tyr Glu Val Leu Glu Ser Gln Lys

1 5 10

<210> 66

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<212> PRT

<213> Bovine sp.

<400> 66

Val Glu Asp Ala Leu His Gln Leu His Ala Arg

1 5 10

<210> 67

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<212> PRT

<213> Bovine sp.

<400> 67

Asp Val Asp Leu Tyr Gln Val Arg

1 5

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Ser Asp Val Gln Glu  
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<400> 71  
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<210> 72  
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<210> 73  
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<220>  
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<210> 74  
<211> 23  
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<220>  
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<400> 74  
catgggacgac aggttccgag acc 23

<210> 75  
<211> 9  
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<400> 75

Lys Gly Ile Pro Ser Phe Trp Leu Thr  
1 5

<210> 76

<211> 9

<212> PRT

<213> Saccharomyces sp.

<400> 76

Lys Gly Ile Pro Glu Phe Trp Leu Thr  
1 5

<210> 77

<211> 10

<212> PRT

<213> Homo sapiens

<400> 77

Asp Ser Phe Phe Asn Phe Phe Ala Pro Pro  
1 5 10

<210> 78

<211> 9

<212> PRT

<213> Saccharomyces sp.

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Glu Ser Phe Phe Asn Phe Phe Ser Pro  
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<210> 79

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<400> 79



Glu Xaa Xaa Lys Glu Xaa Pro Glu Val Lys Xaa Glu Glu Lys  
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<210> 80  
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<400> 80  
Gly Arg Lys Lys Arg  
1 5

<210> 81  
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<400> 81  
Lys Lys Lys Arg Lys  
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<210> 82  
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<210> 83  
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<210> 84  
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<210> 85  
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<210> 86  
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<210> 87  
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<210> 88  
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<210> 89  
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<210> 90  
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<400> 90  
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<210> 91  
<211> 117  
<212> DNA  
<213> Homo sapiens

<400> 91  
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tcggctgata gtggcatgat tgaaccagtg gtcaatgctg tgtccatcca tcaggtg 117

<210> 92

<211> 31

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer C1

<400> 92

ctcagatcta tgggagatac agtagtggag c 31

<210> 93

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer C2

<400> 93

tcgagatctt cacatgatgc cgttggtgag 30

<210> 94

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: P1 Primer

<400> 94

gatttgctgct caataatcac tatctgaa 28

<210> 95

<211> 33

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: P2 Primer

<400> 95

ggttactagg atcacaaagt atgaattctg gaa

33

<210> 96

<211> 5

<212> PRT

<213> HIV-1

<400> 96

Tyr Arg Lys Lys Arg

1

5